

10/525365

DT01 Rec'd PCT/EP 23 FEB 2005

SEQUENCE LISTING

<110> RIKEN et al

<120> Chromo protein and fluorescent protein

<130> 35

<160> A31519A

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<212> PRT

<213> Anthopleura inornata

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35 40 45

Gly Pro Leu Pro Phe Ala Tyr Asp Thr Leu Thr Pro Cys Trp Met Tyr

50 55 60

Gly Ser Lys Thr Phe Ile Lys His Thr Ser Gly Ile Pro Asp Tyr Phe

65 70 75 80

Lys Glu Ser Leu Pro Glu Gly Phe Thr Trp Glu Arg Thr Gln Ile Tyr

85 90 95

Glu Asp Gly Gly Cys Leu Thr Ile His Gln Asp Thr Ser Met Gln Gly

100 105 110

Asp Cys Phe Ile Phe Lys Ile Lys Val Ile Gly Thr Asn Phe Pro Ala

115	120	125
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Ala Leu Lys Cys Lys Asp Gly Asn His Leu Thr Cys His Leu Arg Thr		
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Thr Tyr Arg Ser Arg Lys Ala Gly Gln Lys Met Pro Glu Phe His Phe		
180	185	190
Gly Asp His Arg Ile Glu Ile Leu Lys Glu Glu Glu Gln Gly Met Arg		
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Arg Leu Gly His His		

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gga agt aaa acc ttc atc aag cat aca tca gga att ccc gat tac ttc	240		
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aag gag tct ctt cct gaa ggc ttt act tgg gaa aga acg caa atc tac	288		
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gcc ctg aaa tgc aag gat ggc aac cac ctg acg tgc cat ctg cga act	528		

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Thr Tyr Arg Ser Arg Lys Ala Gly Gln Lys Met Pro Glu Phe His Phe  
180 185 190  
ggg gat cat cgt att gag atc ctg aag gaa gaa gaa caa ggc atg cgt 624  
Gly Asp His Arg Ile Glu Ile Leu Lys Glu Glu Glu Gln Gly Met Arg  
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<213> Anthopleura inornata

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 85 90 95  
 Glu Asp Gly Gly Ser Leu Ser Ile His Gln Asp Thr Ser Leu Gln Gly  
 100 105 110  
 Asp Cys Phe Ile Tyr Lys Ile Lys Val Ile Gly Thr Asn Phe Pro Ala  
 115 120 125  
 Asn Gly Pro Val Met Gln Lys Lys Thr Ala Gly Trp Glu Pro Cys Val  
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 Glu Met Leu Tyr Pro Arg Ala Gly Val Leu Cys Gly Gln Ser Leu Met  
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 180 185 190  
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Lys Pro Phe Glu Gly Tyr Gln Val Glu Lys Ile Arg Val Thr Glu Gly
        35           40           45
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Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Ala Pro Cys Cys Ser Tyr
        50           55           60
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Gly Ser Lys Thr Phe Ile Lys His Val Ser Gly Ile Pro Asp Tyr Phe
        65           70           75           80
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          85           90           95
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Glu Asp Gly Gly Ser Leu Ser Ile His Gln Asp Thr Ser Leu Gln Gly
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 145 150 155 160  
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 Thr Tyr Arg Ser Arg Lys Ala Gly Gln Lys Met Pro Glu Phe His Phe  
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 ggg gat cat cgt att gag atc ctg aag gaa gaa gaa caa ggc atg cgt 624  
 Gly Asp His Arg Ile Glu Ile Leu Lys Glu Glu Glu Gln Gly Met Arg  
 195 200 205  
 att gaa caa tac gag gca gcg gtg gcg agg tac tgc gaa gct cca tcc 672  
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<213> Trachyphyllia geoffroyi

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65 70 75 80  
Gln Ser Phe Pro Lys Gly Phe Ser Trp Glu Arg Ser Leu Met Phe Glu  
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Asp Gly Gly Val Cys Ile Ala Thr Asn Asp Ile Thr Leu Lys Gly Asp  
100 105 110  
Thr Phe Phe Asn Lys Val Arg Phe Asp Gly Val Asn Phe Pro Pro Asn  
115 120 125  
Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Ala Ser Thr Glu  
130 135 140  
Lys Met Tyr Leu Arg Asp Gly Val Leu Thr Gly Asp Ile Thr Met Ala  
145 150 155 160  
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Tyr Lys Ser Arg Gln Glu Gly Val Lys Leu Pro Gly Tyr His Phe Val



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	195	200	205												
Lys	Leu	Tyr	Glu	His	Ala	Val	Ala	His	Ser	Gly	Leu	Pro	Asp	Asn	Val
	210	215	220												
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<212> DNA

<213> *Trachyphyllia geoffroyi*

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				20				25					30			
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Pro	Phe	Glu	Gly	Lys	Gln	Ser	Met	Asp	Leu	Val	Val	Lys	Glu	Gly	Ala	
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Pro	Leu	Pro	Phe	Ala	Tyr	Asp	Ile	Leu	Thr	Thr	Ala	Phe	His	Tyr	Gly	
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aag ctg tat gag cat gct gtt gcc cat tct gga ttg ccg gac aac gtc 672

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215

220

aag taa

678

Lys

225

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<213> Trachyphyllia geoffroyi

<400> 7

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15

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25

30

Pro Phe Glu Gly Lys Gln Ser Met Asp Leu Val Val Lys Glu Gly Ala

35

40

45

Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr Gly

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55

60

Asn Arg Val Phe Ala Lys Tyr Pro Asp His Ile Pro Asp Tyr Phe Lys

65

70

75

80

Gln Ser Phe Pro Lys Gly Phe Ser Trp Glu Arg Ser Leu Met Phe Glu

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90

95

Asp Gly Gly Val Cys Ile Ala Thr Asn Asp Ile Thr Leu Lys Gly Asp

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105

110

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 Lys Met Tyr Leu Arg Asp Gly Val Leu Thr Gly Asp Ile Arg Met Glu  
 145 150 155 160  
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 180 185 190  
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 aat gta aac ggg cac cag ttt gtt att gag gga gat gga aaa ggc cat 96

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 cag tcg ttt ccc aaa ggg ttt tct tgg gag cga agc ctg atg ttc gag 288  
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Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asn Met		
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Ala Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe Arg Thr		
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Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Tyr His Phe		
180	185	190
Ile Asp His Cys Ile Glu Ile Leu Ser His Arg Asn Asp Tyr Asn Asn		
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Val Thr Leu Phe Glu His Ala Val Ala Arg Ser Gly Leu Gln Asp Lys		
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Glu Lys Gln Gln Gln		
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<212> DNA

<213> Scolymia Vitiensis

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Lys Pro Lys Glu Gly Thr Gln Thr Ile Glu Leu Lys Val Val Lys Gly
          35          40          45
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Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr
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ggc aac cgg gta ttc gcc aaa tac cca aag gat ata cca aac tat ttc 240
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          65          70          75          80
gag cag tcg ttt cct gag ggg tat tcg tgg gaa cgg agc atg att ttc 288
Glu Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ile Phe
          85          90          95
gaa gac ggg ggc att tgc atc gct aga aac gac ata aca atg gat ggt 336
Glu Asp Gly Gly Ile Cys Ile Ala Arg Asn Asp Ile Thr Met Asp Gly
          100          105          110
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 Asn Gly Pro Val Met Gln Lys Lys Thr Gln Lys Trp Glu Gln Ser Thr  
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 Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asn Met  
 145 150 155 160  
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 Ala Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe Arg Thr  
 165 170 175  
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 Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Tyr His Phe  
 180 185 190  
 ata gat cac tgc ata gag att tta agc cat cgc aac gat tac aac aac 624  
 Ile Asp His Cys Ile Glu Ile Leu Ser His Arg Asn Asp Tyr Asn Asn  
 195 200 205  
 gtt acg ctt ttt gag cat gct gtt gct cgt tct gga ttg cag gac aaa 672  
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<212> PRT

<213> Scolymia Vitiensis

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Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr  
50 55 60  
Gly Asn Arg Val Phe Ala Lys Tyr Pro Lys Asp Ile Pro Asn Tyr Phe  
65 70 75 80  
Glu Gln Ser Phe Pro Lys Gly Tyr Ser Trp Glu Arg Ser Met Ile Phe  
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Glu Asp Gly Gly Ile Cys Ile Ala Arg Asn Asp Ile Thr Met Glu Gly  
100 105 110  
Gly Thr Phe Tyr Asn Lys Val Arg Phe Tyr Gly Val Asn Phe Pro Pro  
115 120 125  
Asn Gly Pro Val Met Gln Lys Lys Thr Gln Lys Trp Glu Pro Ser Thr  
130 135 140  
Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asn Met  
145 150 155 160  
Ala Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe Arg Thr

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Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Tyr His Phe			
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Ile Asp His Cys Ile Glu Ile Leu Ser His His Asn Asp Tyr Asn Asn			
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Val Thr Leu Phe Glu His Ala Val Ala Arg Ser Gly Leu Gln Asp Lys			
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Gly Ser Val Asn Gly His Asp Phe Val Ile Asp Gly Leu Gly Ser Gly
20 25 30
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Lys Pro Lys Glu Gly Thr Gln Thr Ile Glu Leu Lys Val Val Lys Gly
35 40 45
gga cct tta cct ttc gcc tac gat atc ctg aca aca gca ttc cat tac 192
Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr

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gaa gac ggg ggc att tgc atc gcc aga aac gac ata aca atg gaa ggt 336			
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Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asn Met			
145	150	155	160
gct ctg ttg ctt aaa ggg ggt ggc cat tac cga tgt gac ttc aga act 528			
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	165	170	175
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Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Tyr His Phe			
	180	185	190
ata gat cac tgc ata gag att tta agc cat cac aac gat tac aac aac 624			

Ile Asp His Cys Ile Glu Ile Leu Ser His His Asn Asp Tyr Asn Asn  
195 200 205  
gtt acg ctt ttt gag cat gct gtt gct cgt tct gga ttg cag gac aaa 672  
Val Thr Leu Phe Glu His Ala Val Ala Arg Ser Gly Leu Gln Asp Lys  
210 215 220  
gag aaa caa caa caa tga 690  
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<213> Scolymia Vitiensis

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Glu Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ile Phe  
85 90 95

Glu Asp Gly Gly Ile Cys Ile Ala Arg Asn Asp Ile Thr Met Asp Gly  
 100 105 110  
 Gly Thr Phe Tyr Asn Lys Val Arg Phe Tyr Gly Val Asn Phe Pro Pro  
 115 120 125  
 Asn Gly Pro Val Met Gln Lys Lys Thr Gln Lys Trp Glu Gln Ser Thr  
 130 135 140  
 Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asn Met  
 145 150 155 160  
 Ala Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe Arg Thr  
 165 170 175  
 Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Tyr His Phe  
 180 185 190  
 Ile Asp His Cys Met Glu Ile Leu Ser His Arg Asn Asp Tyr Asn Asn  
 195 200 205  
 Val Thr Leu Phe Glu His Ala Val Ala Arg Ser Gly Leu Gln Asp Lys  
 210 215 220  
 Glu Lys Gln Gln Gln  
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<210> 14

<211> 690

<212> DNA

<213> Scolymia Vitiensis

<400> 14

atg gtg agt gtg att aag gac gaa atg aaa gtc aac ctg cgt atg gaa 48  
 Met Val Ser Val Ile Lys Asp Glu Met Lys Val Asn Leu Arg Met Glu

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ggc agt gta aac gga cac gac ttc gtg att gac gga ctt ggt tca ggc 96			
Gly Ser Val Asn Gly His Asp Phe Val Ile Asp Gly Leu Gly Ser Gly			
20	25	30	
aag cct aaa gag gga aca cag act att gag ctt aaa gtc gta aag ggt 144			
Lys Pro Lys Glu Gly Thr Gln Thr Ile Glu Leu Lys Val Val Lys Gly			
35	40	45	
gga cct tta cct ttc gcc tac gat atc ctg aca aca gca ttc cat tac 192			
Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr			
50	55	60	
ggc aac cgg gta ttc gcc aaa tac cca aag gat ata cca aac tat ttc 240			
Gly Asn Arg Val Phe Ala Lys Tyr Pro Lys Asp Ile Pro Asn Tyr Phe			
65	70	75	80
gag cag tcg ttt cct gag ggg tat tcg tgg gaa cgg agc atg att ttc 288			
Glu Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ile Phe			
85	90	95	
gaa gac ggg ggc att tgc atc gct aga aac gac ata aca atg gat ggt 336			
Glu Asp Gly Gly Ile Cys Ile Ala Arg Asn Asp Ile Thr Met Asp Gly			
100	105	110	
ggc act ttc tat aat aaa gtt cga ttt tat ggt gta aat ttc ccc ccc 384			
Gly Thr Phe Tyr Asn Lys Val Arg Phe Tyr Gly Val Asn Phe Pro Pro			
115	120	125	
aat ggt cca gtt atg cag aag aag acg cag aaa tgg gag caa tcc act 432			
Asn Gly Pro Val Met Gln Lys Lys Thr Gln Lys Trp Glu Gln Ser Thr			
130	135	140	
gag aaa atg tat gcg cgt gat gga gtg ttg acg ggt gat att aac atg 480			





20	25	30
Lys Pro Lys Glu Gly Thr Gln Thr Ile Glu Leu Lys Val Val Lys Gly		
35	40	45
Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr		
50	55	60
Gly Asn Arg Val Phe Ala Lys Tyr Pro Lys Asp Ile Pro Asn Tyr Phe		
65	70	75
Glu Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ile Phe		
	85	90
Glu Asp Gly Gly Ile Cys Ile Ala Arg Asn Asp Ile Thr Met Asp Gly		
100	105	110
Gly Thr Phe Tyr Asn Lys Val Arg Phe Glu Gly Val Asn Phe Pro Pro		
115	120	125
Asn Gly Pro Val Met Gln Lys Asn Thr Leu Lys Trp Glu Pro Ser Thr		
130	135	140
Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asp Met		
145	150	155
Ser Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe Arg Thr		
	165	170
Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Thr His Tyr		
180	185	190
Ile Asp His Ser Ile Glu Ile Leu Ser His Arg Asn Asp Tyr Asn Asn		
195	200	205
Val Thr Leu Phe Glu His Ala Val Ala Arg Ser Gly Leu Gln Asp		
210	215	220

<210> 16

<211> 672

<212> DNA

<213> Scolymia Vitiensis

<400> 16

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Met Val Ser Val Ile Lys Asp Glu Met Lys Val Arg Leu Arg Met Glu
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ggc agt gta aac gga cac gac ttc gtg att gac gga act ggt tca ggc 96
Gly Ser Val Asn Gly His Asp Phe Val Ile Asp Gly Thr Gly Ser Gly
              20              25              30
aag cct aaa gag gga aca cag act att gag ctt aaa gtc gta aag ggt 144
Lys Pro Lys Glu Gly Thr Gln Thr Ile Glu Leu Lys Val Val Lys Gly
              35              40              45
gga cct tta cct ttc gcc tac gat atc ctg aca aca gca ttc cat tac 192
Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr
              50              55              60
ggc aac cgg gta ttc gcc aaa tac cca aag gat ata cca aac tat ttc 240
Gly Asn Arg Val Phe Ala Lys Tyr Pro Lys Asp Ile Pro Asn Tyr Phe
              65              70              75              80
gag cag tcg ttt cct gag ggg tat tcg tgg gaa cgg agc atg att ttc 288
Glu Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ile Phe
              85              90              95
gaa gac ggg ggc att tgc atc gct aga aac gac ata aca atg gat ggt 336
Glu Asp Gly Gly Ile Cys Ile Ala Arg Asn Asp Ile Thr Met Asp Gly
              100             105             110
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ggc act ttc tat aat aaa gtt cga ttt gaa ggt gta aat ttc ccc ccc 384  
 Gly Thr Phe Tyr Asn Lys Val Arg Phe Glu Gly Val Asn Phe Pro Pro  
 115 120 125  
 aat ggt cca gtt atg cag aag aat acg ctg aaa tgg gag cca tcc act 432  
 Asn Gly Pro Val Met Gln Lys Asn Thr Leu Lys Trp Glu Pro Ser Thr  
 130 135 140  
 gag aaa atg tat gcg cgt gat gga gtg ttg acg ggt gat att gac atg 480  
 Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asp Met  
 145 150 155 160  
 tcc ctg ttg ctt aaa ggg ggt ggc cat tac cga tgt gac ttc aga act 528  
 Ser Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe Arg Thr  
 165 170 175  
 act ttc aaa gct aag gag aag ggt gtc aag ttg cca ggc acc cac tac 576  
 Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Thr His Tyr  
 180 185 190  
 ata gat cac agc ata gag att tta agc cat cgc aac gat tac aac aac 624  
 Ile Asp His Ser Ile Glu Ile Leu Ser His Arg Asn Asp Tyr Asn Asn  
 195 200 205  
 gtt acg ctt ttt gag cat gct gtt gct cgt tct gga ttg cag gac taa 672  
 Val Thr Leu Phe Glu His Ala Val Ala Arg Ser Gly Leu Gln Asp  
 210 215 220

<210> 17

<211> 223

<212> PRT

<213> Scolymia Vitiensis

<400> 17

Met Val Ser Val Ile Lys Asp Glu Met Lys Val Arg Leu Arg Met Glu  
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20 25 30  
Lys Pro Lys Glu Gly Thr Gln Thr Ile Glu Leu Lys Val Val Lys Gly  
35 40 45  
Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr  
50 55 60  
Gly Asn Arg Val Phe Ala Lys Tyr Pro Lys Asp Ile Pro Asn Tyr Phe  
65 70 75 80  
Glu Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Thr Phe  
85 90 95  
Glu Asp Gly Gly Val Cys Thr Ala Arg Asn Asp Ile Thr Met Asp Gly  
100 105 110  
Gly Thr Phe Tyr Asn Lys Val Arg Phe Glu Gly Thr Asn Phe Pro Pro  
115 120 125  
Asn Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Pro Ser Thr  
130 135 140  
Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asp Met  
145 150 155 160  
Ser Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Met Arg Thr  
165 170 175  
Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Thr His Tyr  
180 185 190  
Ile Asp His Ser Ile Glu Ile Leu Ser His Arg Asn Asp Tyr Asn Asn

195 200 205  
Val Thr Leu Tyr Glu His Ala Val Ala Arg Ser Gly Leu Gln Asp

210 215 220

<210> 18

<211> 672

<212> DNA

<213> Scolymia Vitiensis

<400> 18

atg gtg agt gtg att aag gac gaa atg aaa gtc cgc ctg cgt atg gaa 48

Met Val Ser Val Ile Lys Asp Glu Met Lys Val Arg Leu Arg Met Glu

1 5 10 15

ggc agt gta aac gga cac gac ttc gtg att gac gga act ggt tca ggc 96

Gly Ser Val Asn Gly His Asp Phe Val Ile Asp Gly Thr Gly Ser Gly

20 25 30

aag cct aaa gag gga aca cag act att gag ctt aaa gtc gta aag ggt 144

Lys Pro Lys Glu Gly Thr Gln Thr Ile Glu Leu Lys Val Val Lys Gly

35 40 45

gga cct tta cct ttc gcc tac gat atc ctg aca aca gca ttc cat tac 192

Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr

50 55 60

ggc aac cgg gta ttc gcc aaa tac cca aag gat ata cca aac tat ttc 240

Gly Asn Arg Val Phe Ala Lys Tyr Pro Lys Asp Ile Pro Asn Tyr Phe

65 70 75 80

gag cag tcg ttt cct gag ggg tat tcg tgg gaa cgg agc atg act ttc 288

Glu Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Thr Phe

85	90	95	
gaa gac ggg ggc gtt tgc acc gct aga aac gac ata aca atg gat ggt 336			
Glu Asp Gly Gly Val Cys Thr Ala Arg Asn Asp Ile Thr Met Asp Gly			
100	105	110	
ggc act ttc tat aat aaa gtt cga ttt gaa ggt aca aat ttc ccc ccc 384			
Gly Thr Phe Tyr Asn Lys Val Arg Phe Glu Gly Thr Asn Phe Pro Pro			
115	120	125	
aat ggt cca gtt atg cag aag aag acg ctg aaa tgg gag cca tcc act 432			
Asn Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Pro Ser Thr			
130	135	140	
gag aaa atg tat gcg cgt gat gga gtg ttg acg ggt gat att gac atg 480			
Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asp Met			
145	150	155	160
tcc ctg ttg ctt aaa ggg ggt ggc cat tac cga tgt gac atg aga act 528			
Ser Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Met Arg Thr			
165	170	175	
act ttc aaa gct aag gag aag ggt gtc aag ttg cca ggc acc cac tac 576			
Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Thr His Tyr			
180	185	190	
ata gat cac agc ata gag att tta agc cat cgc aac gat tac aac aac 624			
Ile Asp His Ser Ile Glu Ile Leu Ser His Arg Asn Asp Tyr Asn Asn			
195	200	205	
gtt acg ctt tat gag cat gct gtt gct cgt tct gga ttg cag gac taa 672			
Val Thr Leu Tyr Glu His Ala Val Ala Arg Ser Gly Leu Gln Asp			
210	215	220	

<210> 19

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 19

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21

<210> 20

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

<400> 20

acvggdccat ydgvaagaaa rtt

23

<210> 21

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

<400> 21

ggccacgcgt cgactagtac gggiigggii gggiig

36

<210> 22

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

<400> 22

aagagactcc ttgaagtaat cggga 25

<210> 23

<211> 20

<212> DNA

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<223> Description of Artificial Sequence: Synthetic DNA

<400> 23

ggccacgcgt cgactagtac 20

<210> 24

<211> 20

<212> DNA

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<223> Description of Artificial Sequence: Synthetic DNA

<400> 24



aaaatatcgt acgcaaaggg 20

<210> 25

<211> 20

<212> DNA

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<223> Description of Artificial Sequence: Synthetic DNA

<400> 25

aggaggtccg ctaccctttg 20

<210> 26

<211> 33

<212> DNA

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<223> Description of Artificial Sequence: Synthetic DNA

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cccggatccg accatggcta ccttggttaa aga 33

<210> 27

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

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<210> 28

<211> 23

<212> DNA

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<223> Description of Artificial Sequence: Synthetic DNA

<400> 28

acvggdccat ydgvaagaaa rtt 23

<210> 29

<211> 36

<212> DNA

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<223> Description of Artificial Sequence: Synthetic DNA

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<210> 30

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

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agttcacacc atgatattca atatcata 28

<210> 31

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

<400> 31

ggccacgcgt cgactagtac 20

<210> 32

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 32

tcttcgtaag tcatgcttcg ttc 23

<210> 33

<211> 21

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

<400> 33

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21

<210> 34

<211> 40

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

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40

<210> 35

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 35

ccgctcgagt tgttgttggtt tctctttgtc ctg

33